

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 26, 2002, 21:05:33 : Search time 27 Seconds
(without alignments)
1480.068 Million cell updates/sec

Title: US-09-840-795-19
Perfect score: 1273
Sequence: 1 MDCQENEYWDQMGRCVTCOR.....AQLFSLDSVPIPGQGGPEM 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhcc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1132	88.9	297	Q9HAV5	Q9HAV5 homo sapien
2	485	38.1	423	Q9NZV2	Q9NZV2 homo sapien
3	483	37.9	417	Q9BY00	Q9BY00 homo sapien
4	483	37.9	423	Q9NS68	Q9NS68 homo sapien
5	480	37.7	423	Q9BX29	Q9BX29 homo sapien
6	478	37.5	348	Q9QXW7	Q9QXW7 mus musculu
7	478	37.5	416	Q9JUH6	Q9JUH6 mus musculu
8	478	37.5	416	Q9JUL3	Q9JUL3 mus musculu
9	474	37.2	214	Q9JHF1	Q9JHF1 mus musculu
10	406	31.9	150	Q9JIL2	Q9JIL2 mus musculu
11	199.5	15.7	448	Q9UNE0	Q9UNE0 homo sapien
12	192.5	15.1	448	Q9UND9	Q9UND9 homo sapien
13	183.5	13.4	448	Q9N187	Q9N187 mus musculu
14	166.5	13.1	514	Q90VY2	Q90VY2 oryzae lat
15	164.5	12.9	514	Q90Z36	Q90Z36 oryzae lat
16	157.5	12.4	186	Q911R5	Q911R5 vaccinia vi

17	156.5	12.3	186	12	Q72735	Q72735 cowpox viru
18	153.5	12.1	186	12	Q9WJB4	Q9WJB4 vaccinia vi
19	150.5	11.8	186	12	Q9YB87	Q9YB87 cowpox viru
20	148	11.6	438	13	Q9DFV0	Q9DFV0 brachydanio
21	145.5	11.4	276	13	Q9DD02	Q9DD02 gallus gall
22	145	11.4	283	6	Q9XS28	Q9XS28 cercopithe
23	143.5	11.3	430	6	Q9N092	Q9N092 macaca fasc
24	141.5	11.1	283	4	Q96J31	Q96J31 homo sapien
25	141	11.1	302	13	Q9PUS0	Q9PUS0 salvelinus
26	140.5	11.0	175	12	Q9PZR3	Q9PZR3 human cytom
27	140.5	11.0	430	4	Q96J01	Q96J01 homo sapien
28	140.5	11.0	430	4	Q969Z4	Q969Z4 homo sapien
29	137.5	10.8	327	6	Q97491	Q97491 ovis aries
30	137	10.8	350	12	Q57116	Q57116 cowpox viru
31	135.5	10.6	175	12	Q9PZS0	Q9PZS0 human cytom
32	135.5	10.6	347	12	Q57115	Q57115 cowpox viru
33	133	10.4	176	12	Q9PZR2	Q9PZR2 human cytom
34	133	10.4	387	13	Q9PYD4	Q9PYD4 xenopus lae
35	132.5	10.4	349	12	Q57305	Q57305 cowpox viru
36	132.5	10.4	355	12	Q85308	Q85308 unidentified
37	132.5	10.4	425	4	Q16042	Q16042 homo sapien
38	132	10.4	176	12	Q9PZR8	Q9PZR8 human cytom
39	131	10.3	433	11	Q912M6	Q912M6 rattus norv
40	131	10.3	461	11	Q91V30	Q91V30 rattus norv
41	130	10.2	176	12	Q9PZR9	Q9PZR9 human cytom
42	130	10.2	461	11	Q91Y93	Q91Y93 rattus norv
43	129.5	10.2	327	11	Q9DCQ1	Q9DCQ1 mus musculu
44	129.5	10.2	331	6	Q9TSM4	Q9TSM4 macaca fasc
45	129.5	10.2	331	6	Q9BDN0	Q9BDN0 macaca neme

ALIGNMENTS

RESULT 1
Q9HAV5 PRELIMINARY: PRT: 297 AA.
ID Q9HAV5
AC Q9HAV5:
DT 01-MAR-2001 (TREMBL) 16, Created
DT 01-MAR-2001 (TREMBL) 16, Last sequence update
DT 01-JUN-2001 (TREMBL) 17, Last annotation update
DE X-LINKED ECTODYSPLASIN-A2 RECEPTOR.
GN XEDAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20495245; PubMed-11039935;
RA Yan M., Wang L.C., Hymowitz S.G., Schilbach S., Lee J., Goddard A.,
RT "Two-amino acid molecular switch in an epithelial morphogen that
RT regulates binding to two distinct receptors."
RL Science 290:523-527(2000).
DR EMBL: AF298812; AAC28761.1;
DR InterPro: IPR001368; TNFR_C6.
DR Pfam: PF00020; TNFR_C6; 2.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS00650; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 297 AA: 32728 MW: 057112766C48240C CRC64;
Query Match 88.9%; Score 1132; DB 4; Length 297;
Best Local Similarity 99.5%; Pred. No. 4,7e-114;
Matches 204; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDCQENEYWDQMGRCVTCORCGPQGLSKDCGGBGAGATCTACPPRRYKSKWGHKQCS 60
|||||
DB 1 MDCQENEYWDQMGRCVTCORCGPQGLSKDCGGBGAGATCTACPPRRYKSKWGHKQCS 60
|||||
OY 61 CITCAVINRQKVNCTATSNVCGDCPLRFYRKTRIGLQDQECIPCKKPTSEVQCAF 120

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Db 61 CITCAVINRQKVCATSNVAGCDCLPREYRKRTRIGLQDOECICTKQPTSEVQCAF 120
OY 121 QLSLVEADAPVPPQEAFTVALVSSLLVFTLAFGLFLFYCKQFFNRHCQRGGLQFEA 180
Db 121 QLSLVEADAPVPPQEAFTVALVSSLLVFTLAFGLFLFYCKQFFNRHCQRGGLQFEA 180
OY 181 DKTAKESLFPVPPEKTSASQVS 205
Db 181 DKTAKESLFPVPPEKTSASQVS 205

RESULT 2
O9NZV2 PRELIMINARY; PRT; 423 AA.
AC Q9NZV2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE TAJ-ALPHA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20270246; PubMed=10809768;
RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-
RT Independent Cell Death.";
RL J. Biol. Chem. 275:15336-15342(2000).
DR EMBL; AF167555; AAF71828.1; -.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 423 AA; 46071 MW; BB7C9917132A4B2F CRC64;

Query Match 38.1%; Score 485; DB 4; Length 423;
Best Local Similarity 44.9%; Pred. No. 5e-44;
Matches 88; Conservative 29; Mismatches 79; Indels 0; Gaps 0;

OY 2 DCOENFYWDQRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSMGHHKQSC 61
Db 33 DCRQOEFRRDSGNCVPCNOCGPGMELSKDCGFYGEDAQCVCRLHREKEDWGFOCKPC 92
OY 62 ITCAVINRQKVCATSNVAGCDCLPREYRKRTRIGLQDOECICTKQPTSEVQCAFQ 121
Db 93 LDCAVNRFQKANCSTSDALICGDCLPGRYRKTGLVGFQDMCVPCGDPPEYEPHCASK 152
OY 122 LSLVEADAPVPPQEAFTVALVSSLLVFTLAFGLFLFYCKQFFNRHCQRGGLQFEAD 181
Db 153 VNLVFIASYPSPRTALAAVICSALATVLLILICVYICKRQPMKKPSMSLSQDIO 212
OY 182 KTKAKESLFPVPPEKTSASQVS 205
Db 213 YNTELSCEFDRLQHE 228

RESULT 3
O9BY00 PRELIMINARY; PRT; 417 AA.
AC O9BY00;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-OCT-2001 (TREMBlrel. 16, Last annotation update)
DE TRDEALPHA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;

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RN [1]
RP SEQUENCE FROM N.A.
RA Chaudhary D., Long A.J.;
RT "TRADE, a novel TNF receptor family member associated with death
RT signaling.";
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF246998; AAK28395.1; -.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 417 AA; 45319 MW; 3AA85D7827AB35C4 CRC64;

Query Match 37.9%; Score 483; DB 4; Length 417;
Best Local Similarity 44.4%; Pred. No. 8.1e-44;
Matches 87; Conservative 29; Mismatches 80; Indels 0; Gaps 0;

OY 2 DCOENFYWDQRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSMGHHKQSC 61
Db 33 DCRQOEFRRDSGNCVPCNOCGPGMELSKDCGFYGEDAQCVCRLHREKEDWGFOCKPC 92
OY 62 ITCAVINRQKVCATSNVAGCDCLPREYRKRTRIGLQDOECICTKQPTSEVQCAFQ 121
Db 93 LDCAVNRFQKANCSTSDALICGDCLPGRYRKTGLVGFQDMCVPCGDPPEYEPHCASK 152
OY 122 LSLVEADAPVPPQEAFTVALVSSLLVFTLAFGLFLFYCKQFFNRHCQRGGLQFEAD 181
Db 153 VNLVFIASYPSPRTALAAVICSALATVLLILICVYICKRQPMKKPSMSLSQDIO 212
OY 182 KTKAKESLFPVPPEKTSASQVS 205
Db 213 YNTELSCEFDRLQHE 228

RESULT 4
O9NS68 PRELIMINARY; PRT; 423 AA.
AC O9NS68;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HTROY.
GN HTROY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20347167; PubMed=10764796;
RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Senba E., Kitamura T.;
RT "HTROY, a newly identified member of the tumor necrosis factor receptor
RT superfamily, exhibits a homology with Eder and is expressed in
RT embryonic skin and hair follicles.";
RL J. Biol. Chem. 275:20742-20747(2000).
DR EMBL; AB040434; BAB03269.1; -.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 423 AA; 46015 MW; B5891CEA9ED45361 CRC64;

Query Match 37.9%; Score 483; DB 4; Length 423;
Best Local Similarity 44.4%; Pred. No. 8.2e-44;
Matches 87; Conservative 29; Mismatches 80; Indels 0; Gaps 0;

OY 2 DCOENFYWDQRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSMGHHKQSC 61
Db 33 DCRQOEFRRDSGNCVPCNOCGPGMELSKDCGFYGEDAQCVCRLHREKEDWGFOCKPC 92

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Best Local Similarity 40.4%; Pred. No. 2.8e-43;
Matches 84; Conservative 30; Mismatches 66; Indels 28; Gaps 1;

QY 2 DCOENEMYDQMGRCVTCORCGPQELSKDCGYEGGDATACPPRRYKSSGHHKQSC 61
D 33 DCRQDEFKDRSGNVCVLCQCGPQELSKDCGYEGGDATACPPRRYKSSGHHKQSC 92
QY 62 ITCAVINRVQKVNCTATSNVAGDCLPRFYKRTKIGLQDECIPTCKQPTSEVOCARQ 121
D 93 ADCALVNRFPQRANCSHTSDAVCGDCLPGFYKRTKIGLQDECIPTCKQPTSEVOCARQ 152
QY 122 LSLVEADAPVPPOEATLVALVSSLLVFTLAFGLFELYCKQFNN----- 167
D 153 VNLVKISSTVSSPRDTALAATVCSALATVLLALILCVIYCKRQFMKKRPSMSLRSDIQ 212
QY 168 -----RHCGRGGLQFEAD 181
D 213 YNGSELSCFDQPRLRHCAHRACQYHRD 240

RESULT 8

09JUL3 PRELIMINARY; PRT; 416 AA.
AC 09JUL3: 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TAJ-ALPHA LONG.
GN TNFRSF19.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20270246; PubMed=10809768;
RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-
RT Independent Cell Death.";
RL J. Biol. Chem. 275:15336-15342(2000).
DR EMBL; AF167552; AAF71825.1;
DR MGI; MGI:1352474; Tnftrsf19.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00202; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS00650; TNFR_NGFR_2; 1.
SQ SEQUENCE 416 AA; 45294 MW; 19CA2F75DD7B9D49 CRC64;

Query Match 37.5%; Score 478; DB 11; Length 416;
Best Local Similarity 40.4%; Pred. No. 2.8e-43;
Matches 84; Conservative 30; Mismatches 66; Indels 28; Gaps 1;

QY 2 DCOENEMYDQMGRCVTCORCGPQELSKDCGYEGGDATACPPRRYKSSGHHKQSC 61
D 33 DCRQDEFKDRSGNVCVLCQCGPQELSKDCGYEGGDATACPPRRYKSSGHHKQSC 92
QY 62 ITCAVINRVQKVNCTATSNVAGDCLPRFYKRTKIGLQDECIPTCKQPTSEVOCARQ 121
D 93 ADCALVNRFPQRANCSHTSDAVCGDCLPGFYKRTKIGLQDECIPTCKQPTSEVOCARQ 152
QY 122 LSLVEADAPVPPOEATLVALVSSLLVFTLAFGLFELYCKQFNN----- 167
D 153 VNLVKISSTVSSPRDTALAATVCSALATVLLALILCVIYCKRQFMKKRPSMSLRSDIQ 212
QY 168 -----RHCGRGGLQFEAD 181
D 213 YNGSELSCFDQPRLRHCAHRACQYHRD 240

RESULT 9

09JUL3

ID 09JUL3 PRELIMINARY; PRT; 214 AA.
AC 09JUL3: 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DTROY (TAJ-ALPHA SHORT).
GN TNFRSF19 OR DTROY.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20347167; PubMed=10764796;
RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Senba E., Kitamura T.;
RT "TRDY, a newly identified member of the tumor necrosis factor receptor
RT superfamily, exhibits a homology with Edar and is expressed in
RT embryonic skin and hair follicles.";
RL J. Biol. Chem. 275:20742-20747(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20270246; PubMed=10809768;
RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-
RT Independent Cell Death.";
RL J. Biol. Chem. 275:15336-15342(2000).
DR EMBL; AB040433; BAB03268.1;
DR EMBL; AF167553; AAF71826.1;
DR MGI; MGI:1352474; Tnftrsf19.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00202; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS00650; TNFR_NGFR_2; 1.
SQ SEQUENCE 214 AA; 23564 MW; ECC63981C37482B8 CRC64;

Query Match 37.2%; Score 474; DB 11; Length 214;
Best Local Similarity 47.9%; Pred. No. 3.6e-43;
Matches 79; Conservative 29; Mismatches 57; Indels 0; Gaps 0;

QY 2 DCOENEMYDQMGRCVTCORCGPQELSKDCGYEGGDATACPPRRYKSSGHHKQSC 61
D 33 DCRQDEFKDRSGNVCVLCQCGPQELSKDCGYEGGDATACPPRRYKSSGHHKQSC 92
QY 62 ITCAVINRVQKVNCTATSNVAGDCLPRFYKRTKIGLQDECIPTCKQPTSEVOCARQ 121
D 93 ADCALVNRFPQRANCSHTSDAVCGDCLPGFYKRTKIGLQDECIPTCKQPTSEVOCARQ 152
QY 122 LSLVEADAPVPPOEATLVALVSSLLVFTLAFGLFELYCKQFNN----- 166
D 153 VNLVKISSTVSSPRDTALAATVCSALATVLLALILCVIYCKRQFNN----- 197

RESULT 10
09JUL3 PRELIMINARY; PRT; 150 AA.
AC 09JUL3: 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TAJ-BETA1.
GN TNFRSF19.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20270246; PubMed=10809768;
RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,

RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-
 RT Independent Cell Death."
 RL J. Biol. Chem. 275:15336-15342(2000).
 DR EMBL: AF167554; AAF71827.1; -
 DR MGD: MGI:1352474; Tnfrsf19.
 DR InterPro: IPR001368; TNER_c6.
 DR Pfam: PF00020; TNER_c6; 2.
 DR SMART: SM00208; TNER; 2.
 DR PROSITE: PS00652; TNER_NGFR.1; UNKNOWN_2.
 DR PROSITE: PS50050; TNER_NGFR.2; 1.
 SO SEQUENCE 150 AA; 16728 MW; 4A1B2E93AE7FF43 CRC64;

Query Match 31.9%; Score 406; DB 11; Length 150;
 Best Local Similarity 54.7%; Pred. No. 5.3e-36;
 Matches 64; Conservative 18; Mismatches 35; Indels 0; Gaps 0;

QY 2 DCOENYWDQWGRVCYQRCRGPGQELSKDCGYEGGDAYCTACPPRRYKSSWGHKQSC 61
 DB 33 DCRQGERDRKNCVILKQCGPMELSKGCGYGEDACVCPRPKRKEDMGFOCKKPC 92
 QY 62 ITCAVIRVOKNCTATSNVAVCGDCLPFRYKRTIGLQDOECJPCTKQPTSEVQC 118
 DB 93 ADCALVNRFORANCSSHSDAVCGDCLPFRYKRTIGLQDOECJPCTKQPTSEVQC 149

RESULT 11

Q9UNE0 PRELIMINARY; PRT; 448 AA.
 ID Q9UNE0;
 AC Q9UNE0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ECTODYSPLASIN-A RECEPTOR PROTEIN.
 GN EDAR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99364416; PubMed=10431241;
 RA Montreal A.W., Ferguson B.M., Headon D.J., Street S.L., Overbeek P.A.,
 RA Zonana J.;
 RT "Mutations in the human homologue of mouse dl cause autosomal
 recessive and dominant hypohidrotic ectodermal dysplasia."
 RL Nat. Genet. 22:366-369(1999).
 DR EMBL: AF130988; AAD50076.1; -
 DR HSSP: P25942; ICDF.
 DR InterPro: IPR000488; Death.
 DR Pfam: PF00531; death; 1.
 KW Receptor.
 SO SEQUENCE 448 AA; 48582 MW; AC8D61249D608439 CRC64;

Query Match 15.7%; Score 199.5; DB 4; Length 448;
 Best Local Similarity 24.9%; Pred. No. 3.6e-13;
 Matches 71; Conservative 33; Mismatches 112; Indels 69; Gaps 14;

QY 2 DCOENYWDQWGRVCYQRCRGPGQELSKDCGYEGGDAYCTACPPRRYKSSWGHKQSC 54
 DB 30 NCGENYNNQTTGLCQCPGPGPEEYLSGCGYTKDEYGCVPAPKFSKGYQICRR 89
 QY 55 HHKQSCITTCVAVIRVOKNCTATSNVAVCGDCLPFRYKRTIGLQDOECJPCTKQPT 113
 DB 90 HKDCGEGFRATVILPQGMEN-----DAECGFCPLPGYMLNRPNNITGMVCYSCLLAPN 144
 QY 114 SEVQCAFQSLVEADAP-----TVPOE-----ATLVAVSSLLVFTLAFL 155
 DB 145 TK-ECVATSGASANFPQTSSSTLSPQHAKELSGGHLATLTIAMSTIFIMATAIV 203
 QY 156 GLPFLY-----CKQFNNHCORGLQFEADTKAKE-----BSLF 190
 DB 204 LIIMFYILKTRKPSAPACC-----TSHPKGSVEAQSVDKEKKEADNVNMFSEKDEFKEL- 258

QY 191 PVPSKETSASQSVSWAPSLAQLFS-----LDSVP1PQ000GPEM 231
 DB 259 TATPAKPTKSENDAS-----SENEQLLSRVSVDDEPAPKQSGPFL 300

RESULT 12

Q9UND9 PRELIMINARY; PRT; 448 AA.
 ID Q9UND9;
 AC Q9UND9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ECTODYSPLASIN-A RECEPTOR PROTEIN.
 GN EDAR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99364416; PubMed=10431241;
 RA Montreal A.W., Ferguson B.M., Headon D.J., Street S.L., Overbeek P.A.,
 RA Zonana J.;
 RT "Mutations in the human homologue of mouse dl cause autosomal
 recessive and dominant hypohidrotic ectodermal dysplasia."
 RL Nat. Genet. 22:366-369(1999).
 DR EMBL: AF130986; AAD50077.1; -
 DR EMBL: AF130990; AAD50077.1; JOINED.
 DR EMBL: AF130991; AAD50077.1; JOINED.
 DR EMBL: AF130992; AAD50077.1; JOINED.
 DR EMBL: AF130993; AAD50077.1; JOINED.
 DR EMBL: AF130994; AAD50077.1; JOINED.
 DR EMBL: AF130995; AAD50077.1; JOINED.
 DR HSSP: P25942; ICDF.
 DR InterPro: IPR000488; Death.
 DR Pfam: PF00531; death; 1.
 KW Receptor.
 SO SEQUENCE 448 AA; 48572 MW; AC8E80F79CB255EA CRC64;

Query Match 15.1%; Score 192.5; DB 4; Length 448;
 Best Local Similarity 23.1%; Pred. No. 2e-12;
 Matches 66; Conservative 36; Mismatches 113; Indels 71; Gaps 12;

QY 2 DCOENYWDQWGRVCYQRCRGPGQELSKDCGYEGGDAYCTACPPRRYKSSWGHKQSC 54
 DB 30 NCGENYNNQTTGLCQCPGPGPEEYLSGCGYTKDEYGCVPAPKFSKGYQICRR 89
 QY 55 HHKQSCITTCVAVIRVOKNCTATSNVAVCGDCLPFRYKRTIGLQDOECJPCTKQPT 113
 DB 90 HKDCGEGFRATVILPQGMEN-----DAECGFCPLPGYMLNRPNNITGMVCYSCLLAPN 144
 QY 114 SEVQCAFQSLVEADAP-----TVPOE-----ATLVAVSSLLVFTLAFL 155
 DB 145 TK-ECVATSGASANFPQTSSSTLSPQHAKELSGGHLATLTIAMSTIFIMATAIV 203
 QY 156 GLPFLY-----CKQFNNHCORGLQFEADTKAKE-----BSLF 186
 DB 204 LIIMFYILKTRKPSAPACC-----TSHPKGSVEAQSVDKEKKEADNVNMFSEKDEFKEL 259

RESULT 13

Q9RI87 PRELIMINARY; PRT; 448 AA.
 ID Q9RI87;
 AC Q9RI87;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ECTODERMAL DYSPLASIA RECEPTOR.
 GN EDAR OR DL.

Query Match	13.1%;	Score 166.5;	DB 13;	Length 514;
Best Local Similarity	24.5%;	Pred. No. 1.5e-09;		
Matches 54;	Conservative 38;	Mismatches 101;	Indels 27;	Gaps 9

Search completed: October 26, 2002, 21:09:48
Job time : 30 secs